GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24 ; Search time 1703.81 Seconds
(without alignments)
7460.491 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	364.8	69.8	558	9	AI503976	AI503976 vm43d08.x
c	2	363	69.4	623	9	AW146128	AW146128 um37e10.x
c	3	348.2	66.6	549	9	AI169253	AI169253 EST215088
c	4	347	66.3	558	9	AI265629	AI265629 uj04b07.x
	5	339.6	64.9	614	14	CD373004	CD373004 UI-R-GR0-
	6	339.2	64.9	816	9	AI119218	AI119218 ue94h02.y
	7	334.8	64.0	594	10	BF383724	BF383724 602044632
	8	334.4	63.9	796	14	CB959991	CB959991 AGENCOURT
c	9	322.2	61.6	499	9	AW495481	AW495481 UI-M-BH3-
c	10	320.8	61.3	642	9	AI876493	AI876493 uj59b10.x
c	11	320.8	61.3	673	12	BM984670	BM984670 UI-CF-EC1
c	12	316.8	60.6	575	9	AI248089	AI248089 qh69f05.x
c	13	309.2	59.1	468	9	AI169770	AI169770 EST215669
c	14	305	58.3	498	9	AA542914	AA542914 ni98c10.s
	15	299	57.2	882	9	AI604642	AI604642 vm43d08.y
c	16	296.4	56.7	653	13	BQ200567	BQ200567 UI-R-DZ1-
c	17	291.6	55.8	527	9	AA913900	AA913900 ol35g05.s
c	18	271.6	51.9	521	9	AW493459	AW493459 UI-M-BH3-
	19	271.6	51.9	559	12	BI715603	BI715603 ic34h10.y
	20	271.6	51.9	602	13	BU590710	BU590710 AGENCOURT
	21	271.6	51.9	621	12	BI221656	BI221656 602936980
	22	271.6	51.9	1658	11	AK081019	AK081019 Mus muscu
c	23	270.6	51.7	595	9	AI573421	AI573421 mo04b11.x
c	24	270	51.6	499	12	BI676839	BI676839 ic56a08.x
c	25	266.8	51.0	500	9	AA945553	AA945553 EST201052
c	26	266.8	51.0	525	9	AA963258	AA963258 UI-R-E1-g
	27	266	50.9	665	9	AA690767	AA690767 vu57d12.r
	28	265.2	50.7	559	12	BI715465	BI715465 ic33b09.y
	29	263.8	50.4	799	9	AI314558	AI314558 uj48d07.y
c	30	263.6	50.4	525	9	AI599751	AI599751 EST251454
c	31	261.4	50.0	499	12	BI294072	BI294072 UI-R-DK0-
c	32	260.4	49.8	561	12	BI714874	BI714874 ic33b09.x
c	33	258.4	49.4	502	9	AI104669	AI104669 EST213958
c	34	258	49.3	564	12	BI714981	BI714981 ic34h10.x
	35	256	48.9	2170	11	AK038119	AK038119 Mus muscu
c	36	254.8	48.7	430	9	AI478804	AI478804 tm52e04.x
	37	254.8	48.7	558	12	BI715475	BI715475 ic33c08.y
	38	250.8	48.0	512	9	AI876203	AI876203 uj59b10.y
	39	249.6	47.7	949	14	CB589117	CB589117 AGENCOURT
c	40	248.2	47.5	637	9	AW413016	AW413016 uq49h08.x
	41	246.4	47.1	473	9	AA451360	AA451360 vf84g03.r
c	42	246.4	47.1	486	9	AA993659	AA993659 ot85g11.s
	43	246.2	47.1	773	12	BI144500	BI144500 602908689
	44	243.2	46.5	482	9	AA456717	AA456717 aa13h06.r
c	45	243	46.5	474	9	AI526955	AI526955 uj48d07.x

ALIGNMENTS

RESULT 1
AI503976/c
LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999
DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION AI503976
VERSION AI503976.1 GI:4401827
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 558)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:565223
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 440.
FEATURES Location/Qualifiers
source 1. .558
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1001007"
/tissue_type="diaphragm"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse diaphragm (#937303)"
/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT 103 a 133 c 149 g 173 t
ORIGIN

Query Match 69.8%; Score 364.8; DB 9; Length 558;
Best Local Similarity 83.2%; Pred. No. 8.8e-81;
Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        530 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 471

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        470 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 411

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||| ||||||||||||
Db        410 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 351

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  |||||||||||||||||| |||
Db        350 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 291

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        290 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 231

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        230 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 171

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        170 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 111

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |    |||||| | || |||  |||      || |||||||   ||
Db        110 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 51

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||| ||||||| |||||||||||||||||||| ||||||||||||
Db         50 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTC 1
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RESULT 2
AW146128/c

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LOCUS       AW146128                623 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AW146128
VERSION     AW146128.1  GI:6167864
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
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            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1006958
            Seq primer: custom primer used
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .623
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2247498"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse embryo mewa"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers  for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT      123 a    138 c    170 g    191 t      1 others
ORIGIN

  Query Match             69.4%;  Score 363;  DB 9;  Length 623;
  Best Local Similarity   81.9%;  Pred. No. 2.5e-80;
  Matches  433;  Conservative    0;  Mismatches   90;  Indels    6;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || | ||| ||||||||||||||||||||||||||||||||||||||
Db        541 GGACCAGAGACCCTTTTCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 482

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        481 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 422

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||| ||||| ||||||
Db        421 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAAATGTAC 362
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Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  ||||||||||||||||||| |||
Db        361 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 302

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        301 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 242

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||| |||||||||| |||||||||||||| |||
Db        241 AGAAGGAAAGGAAGTACATTTGAAGAACCCAAGTAGAGGAAGTGCAGGAAACAAGACCTA 182

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        181 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 122

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| | ||  ||  |||      || |||||||   ||
Db        121 CTGCTTGAGCAACCTGCAAAACATCGAAACCCCTACCAAATAACAATAATAAGTCCAATA 62

Qy        475 ACATTTCAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||| |||||||||   || ||||||||||||| |||||||||||||
Db         61 ACATTACAAAGATGGGCATTTCCCCAATGAAATATACAAGTAAACATTC 13
```

```
RESULT 3
AI169253/c
LOCUS       AI169253                549 bp    mRNA    linear   EST 08-JAN-1999
DEFINITION  EST215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
            RKIBP33 3' end, mRNA sequence.
ACCESSION   AI169253
VERSION     AI169253.1  GI:4134375
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 549)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished
COMMENT     On Oct 6, 1998 this sequence version replaced gi:3705561.
            Other_ESTs: TC50779
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .549
                     /organism="Rattus sp."
```

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                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
                     /clone="RKIBP33"
                     /clone_lib="Normalized rat kidney, Bento Soares"
                     /note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT      112 a    140 c    133 g    164 t
ORIGIN

  Query Match             66.6%;  Score 348.2;  DB 9;  Length 549;
  Best Local Similarity   81.8%;  Pred. No. 1.3e-76;
  Matches  428;  Conservative    0;  Mismatches   88;  Indels    7;  Gaps    2;

Qy          8 AGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCT 67
              |||| || ||||| |||||||||||||| |||||||| ||||||||||||   |||||||
Db        549 AGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCAAGGGGCT 490

Qy         68 TTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCA 127
              |||| |||||||||||||||| || |||||||||| ||| |||||||| ||||| ||||
Db        489 TTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGAAGGGCACCACAGACGGGCA 430

Qy        128 TCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCAC 187
              | |||||||||||  ||||||||||||||||||||||||||||||||||||||||| |
Db        429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy        188 CCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCA 247
              | || |||||  |||||  |||| || ||| |||| |||||||||||||  ||||||||||
Db        369 CGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGACATGCCCA 310

Qy        248 AGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGA 307
              ||||||||||||  |||||  | |||  ||  |||||||||  ||||   || ||||||||||
Db        309 AGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy        308 AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG 367
              ||||||||||| |||||||||||||||||||  ||||||||||||||||  |||||  |||
Db        249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy        368 TAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCA 427
              |||||  ||  |||  | |||||     | ||  |  ||  |  |||||||  ||  ||||||||
Db        189 TAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 130

Qy        428 CAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCACATTTC 481
                    |    ||||||  ||||  |||  ||||       ||  |||  ||||   ||   ||||||
Db        129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTC 70

Qy        482 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              | ||||  ||||||||||  |||||||||||||||||||||||
Db         69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 27


RESULT 4
AI265629/c
LOCUS       AI265629                 558 bp    mRNA    linear   EST 18-NOV-1998
DEFINITION  uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI265629
```

VERSION AI265629.1 GI:3883787
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 558)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:975225
Seq primer: custom primer used
High quality sequence stop: 495.
FEATURES Location/Qualifiers
source 1. .558
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890901"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
BASE COUNT 106 a 135 c 156 g 161 t
ORIGIN

Query Match 66.3%; Score 347; DB 9; Length 558;
Best Local Similarity 82.0%; Pred. No. 2.5e-76;
Matches 414; Conservative 0; Mismatches 85; Indels 6; Gaps 1;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        506 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 447

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || ||||||||| ||||||||||||||||
Db        446 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 387

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||| ||||||||||||
Db        386 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 327

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  |||||||||||||||||| |||
Db        326 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 267

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        266 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 207

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        206 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 147

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        146 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 87

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| | || |||  |||      || |||||||   ||
Db         86 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 27

Qy        475 ACATTTCAAAGATGGCATTTCCCCC 499
              ||||| |||||||||   || ||||
Db         26 ACATTACAAAGATGGGCATTTCCCC 2
```

```
RESULT 5
CD373004
LOCUS       CD373004                614 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-R-GR0-csv-j-17-0-UI.r1 UI-R-GR0 Rattus norvegicus cDNA clone
            UI-R-GR0-csv-j-17-0-UI 5', mRNA sequence.
ACCESSION   CD373004
VERSION     CD373004.1  GI:31157094
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 614)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
```

COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/rat.html
Seq primer: M13 REVERSE.

FEATURES Location/Qualifiers
source 1. .614
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-GR0-csv-j-17-0-UI"
/tissue_type="Whole embryo"
/dev_stage="embryo 13dpc"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-GR0"
/note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
UI-R-GR0 is a cDNA library containing the following
tissue(s): rat whole embryo 13dpc. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. Denatured RNA was size
fractionated on a 1% agarose gel. First strand cDNA
synthesis was primed with oligo-dT primer containing a Not
I site. Double strand cDNA was size selected according to
mRNA size fraction, ligated with EcoR I adaptor, digested
with NotI and then cloned directionally into pYX-Asc
vector. The library tag sequence located between the Not I
site and the polyA tail is CATCTCTACT. This library was
created for the University of Iowa Program for Rat Gene
Discovery and Mapping (Val Sheffield, Bento Soares and Tom
Casavant)."

BASE COUNT 171 a 168 c 154 g 119 t 2 others
ORIGIN

Query Match 64.9%; Score 339.6; DB 14; Length 614;
Best Local Similarity 81.4%; Pred. No. 1.9e-74;
Matches 393; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db        116 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 175

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| |||||||||||| |||
Db        176 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 235

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||
```

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Db        236 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 295

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  ||||| |||| || ||| |||| ||||||||||||||| |||
Db        296 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 355

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  ||||||||| ||||   || |||
Db        356 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 415

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        416 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 475

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | ||   || | ||||||| || ||||||
Db        476 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATTCCACGTCACCGCATGATCCTTTG 535

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||           |     ||||| |||| ||| |||||| |  ||   |||   || |
Db        536 CTGCTTGAGCAACCTGCANAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 595

Qy        481 CAA 483
              | |
Db        596 CCA 598
```

```
RESULT 6
AI119218
LOCUS       AI119218                816 bp    mRNA    linear   EST 02-SEP-1998
DEFINITION  ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:1498803 5' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI119218
VERSION     AI119218.1  GI:3519542
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
```

```
            MGI:936407
            Seq primer: custom primer used
            High quality sequence stop: 473.
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1498803"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse embryo mewa"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers  for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT      230 a    219 c    172 g    187 t      8 others
ORIGIN

  Query Match             64.9%;  Score 339.2;  DB 9;  Length 816;
  Best Local Similarity   81.2%;  Pred. No. 2.5e-74;
  Matches  389;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        323 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 382

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        383 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 442

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||| ||||||||||||
Db        443 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 502

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  |||||||||||||||||| |||
Db        503 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 562

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        563 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 622

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||| |||||| ||||||||| |||
Db        623 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCANGAAACAAGACCTA 682
```

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Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| ||||| || || ||| |   ||||   |  | | ||   ||||||| || ||||||
Db        683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATT 479
              ||           |     ||||| | || |||  ||||| || |  | | |   || |
Db        743 CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAAT 801


RESULT 7
BF383724
LOCUS       BF383724                 594 bp    mRNA    linear   EST 27-NOV-2000
DEFINITION  602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5',
            mRNA sequence.
ACCESSION   BF383724
VERSION     BF383724.1  GI:11365029
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9527  row: p  column: 08
            High quality sequence stop: 589.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4194295"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Li9"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.9 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      175 a    162 c    142 g    115 t
ORIGIN

  Query Match             64.0%;  Score 334.8;  DB 10;  Length 594;
  Best Local Similarity   82.0%;  Pred. No. 2.9e-73;
  Matches  400;  Conservative    0;  Mismatches   82;  Indels    6;  Gaps    1;

Qy         16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTC 75
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                |||||  ||||||||||||||||||||||||||||||||||||    |||||||||||  |||
Db        107 TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCGAGGGGCTTTTACTTC 166

Qy         76 AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT 135
                |||||||||||||| || ||||||||| ||||||||||||||||||||||| ||||||
Db        167 AACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAGACAGGCATTGTGGAT 226

Qy        136 GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG 195
                |||||  |||||||||||||||||||||||| ||||||||||||||||  || ||  |||
Db        227 GAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTACTGTGCCCCACTGAAG 286

Qy        196 CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG 255
                ||  ||||  ||||||||||  |||||||||||||||||  ||||||||||||||||||
Db        287 CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGACATGCCCAAGACTCAG 346

Qy        256 AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT 315
                ||||  | | | | ||| || |||||||||| ||||   || ||||||||||||||||||
Db        347 AAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGGAGAAGGAAAGGAAGT 406

Qy        316 ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 375
                |||||||||||||||||||||| ||||||||||||||| |||||| |||||||| ||
Db        407 ACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATGTAGGAGGA 466

Qy        376 CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCACAGTTACC 435
                 ||| |   ||||   | || | ||   |||||||||| ||||||||          |
Db        467 GCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTGCTGCTTGAGCAACCT 526

Qy        436 TGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCACATTTCAAAGATGG 489
                  |||||| | || |||  |||      || |||||||   || ||||| |||||||||
Db        527 GCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATAACATTACAAAGATGG 586

Qy        490 CATTTCCC 497
                  || ||
Db        587 GCATTGCC 594
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RESULT 8
CB959991
LOCUS       CB959991                796 bp    mRNA    linear   EST 29-APR-2003
DEFINITION  AGENCOURT_13888044 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30341081 5', mRNA sequence.
ACCESSION   CB959991
VERSION     CB959991.1  GI:30216107
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM371 row: p column: 18
High quality sequence stop: 707.

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FEATURES             Location/Qualifiers
     source          1. .796
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30341081"
                     /tissue_type="Human Placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: This is
                     a NIH_MGC library."
BASE COUNT      224 a    197 c    191 g    184 t
ORIGIN
```

Query Match 63.9%; Score 334.4; DB 14; Length 796;
Best Local Similarity 84.6%; Pred. No. 3.9e-73;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        180 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 239

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        240 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 299

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        300 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 359

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        360 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 419

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        420 ATGCCCAAGACCCAG---------------------------------------------- 434

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        435 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 487

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
```

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                ||||||||||||||||||| ||||||||||||||  |||| ||||||||||||| ||||||
Db        488 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 547

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
                |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
Db        548 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 607

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
                || |||||| ||| ||||||||||||||||||||||||||||||
Db        608 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 653
```

```
RESULT 9
AW495481/c
LOCUS       AW495481                 499 bp    mRNA    linear   EST 24-FEB-2000
DEFINITION  UI-M-BH3-auy-g-11-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
            UI-M-BH3-auy-g-11-0-UI 3', mRNA sequence.
ACCESSION   AW495481
VERSION     AW495481.1  GI:7065762
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized pineal glands library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
```

/clone="UI-M-BH3-auy-g-11-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC"
BASE COUNT 86 a 112 c 124 g 177 t
ORIGIN

Query Match 61.6%; Score 322.2; DB 9; Length 499;
Best Local Similarity 82.3%; Pred. No. 4e-70;
Matches 396; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

```
Qy        50 TGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGA 109
             ||||||||   |||||||||||| |||||||||||||||| || |||||||||| |||||
Db       499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGA 440

Qy       110 GGGCACCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
             |||||||||||||||||| |||||||||| ||||||||||||||||||||||||||| |
Db       439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy       170 TGGAGATGTACTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGC 229
             ||||||||||||||| || || |||||  |||| |||||||||||  ||||||||||||
Db       379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy       230 GCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGA 289
             |||||||  |||||||||||||||||||||  | | | | ||| || |||||||||| ||
Db       319 GCCACACTGACATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy       290 AGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 349
```

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                ||   || ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db          259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA 200

Qy          350 AACAAGAACTACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGC 409
                ||||||| |||||| |||||||| || ||| |   ||||   | || | ||   ||||||
Db          199 AACAAGACCTACAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGC 140

Qy          410 AGGACCCTTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAA 463
                |||| ||||||||           |    |||||| | || |||  |||      || ||
Db          139 AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80

Qy          464 TAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 522
                |||||   || ||||| ||||||| |||||||||||||||||||| ||||||||||||
Db           79 TAAGTCCAATAACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATT 20

Qy          523 C 523
                |
Db           19 C 19
```

```
RESULT 10
AI876493/c
LOCUS       AI876493                642 bp    mRNA    linear   EST 21-JUL-1999
DEFINITION  uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1924219 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI876493
VERSION     AI876493.1  GI:5550542
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:980511
            Seq primer: custom primer used
            High quality sequence stop: 257.
FEATURES             Location/Qualifiers
     source          1. .642
                     /organism="Mus musculus"
                     /mol_type="mRNA"
```

/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1924219"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 127 a 154 c 175 g 185 t 1 others
ORIGIN

Query Match 61.3%; Score 320.8; DB 9; Length 642;
Best Local Similarity 80.1%; Pred. No. 9.6e-70;
Matches 403; Conservative 0; Mismatches 93; Indels 7; Gaps 2;

```
Qy          2 GACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACA 61
              |||| ||||| || ||||| |||||||||||||||||||||||| ||||||||||    |
Db        503 GACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGGTCGTGTGTGGACCGA 444

Qy         62 GGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGA 121
              ||||||||| |||||||||| ||||||| || |||||||||| | ||||||||||||||
Db        443 GGGGCTTTTTCTTCAACAAGGCCACAGGCTATGGCTCCAGCATTTGGAGGGCACCTCAGA 384

Qy        122 CAGGCATCGTGGATGAGTGCTGCTTCCGG-AGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||| ||  |||||||||||| ||||||||| |||||||||||||| || ||| ||||||||
Db        383 CAGTCAATGTGGATGAGTGTTGCTTCCGGAAGCTGTGATCTGAGAAGACTGNAGATGTAC 324

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| |||||||||||  |||||||||||||||||||| |||
Db        323 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 264

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        263 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 204

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        203 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 144

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        143 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 84

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| | || |||  |||      || |||||||   ||
```

```
Db         83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24

Qy        475 ACATTTCAAAGATGGCATTTCCC 497
              ||||| |||||||||   || ||
Db         23 ACATTACAAAGATGGGCATTTCC 1


RESULT 11
BM984670/c
LOCUS       BM984670                673 bp    mRNA    linear   EST 20-FEB-2003
DEFINITION  UI-CF-EC1-abj-k-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.
ACCESSION   BM984670
VERSION     BM984670.1  GI:19610417
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 673)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .673
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-abj-k-24-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
```

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG_LIB=UI-CF-EC1
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_SEQ=AAGTGCTTAC"

BASE COUNT 152 a 164 c 169 g 188 t
ORIGIN

Query Match 61.3%; Score 320.8; DB 12; Length 673;
Best Local Similarity 84.2%; Pred. No. 9.7e-70;
Matches 443; Conservative 0; Mismatches 27; Indels 56; Gaps 5;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        492 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 433

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||| |||||||||| |||||||||||  || ||||||||||||||||||| ||||||
Db        432 AGGGG-TTTTATTTCAGCAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        373 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 254

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db        253 ATGCCCAAGACCCAG---------------------------------------------- 239

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        238 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 186

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| ||||||||||||  |||| ||||||||||| ||||||
Db        185 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 126

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
Db        125 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 66

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||||
Db         65 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 20
```

RESULT 12
AI248089/c
LOCUS AI248089 575 bp mRNA linear EST 01-DEC-1998
DEFINITION qh69f05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849953 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI248089
VERSION AI248089.1 GI:3843486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 575)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 918 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 380.
FEATURES Location/Qualifiers
source 1. .575
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1849953"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 135 a 152 c 131 g 156 t 1 others
ORIGIN

Query Match 60.6%; Score 316.8; DB 9; Length 575;
Best Local Similarity 83.8%; Pred. No. 9.4e-69;
Matches 428; Conservative 0; Mismatches 28; Indels 55; Gaps 4;

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Qy         16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTC 75
              ||||| |||||||||||| |||||||||||||||||||| ||||||||||||||||||
Db        551 TGCGGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGTGAAGACAGGGGCTTTTATTTC 492
```

```
Qy         76 AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT 135
              ||||||||||||| || ||||||||||||||||||| ||||||||||||||||||||
Db        491 AACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGAT 432

Qy        136 GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG 195
              |||||||||||||||||||||||| |||||||||||||||| || ||||||||||||
Db        431 GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 372

Qy        196 CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG 255
              || || ||| |||| ||||| ||||||||||||||||||||||||||||||||||| |||
Db        371 CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAG 312

Qy        256 AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT 315
                                                                ||||||||
Db        311 ----------------------------------------------------AAGGAAGT 304

Qy        316 ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 375
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        303 ACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 244

Qy        376 CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCAC-AGTTAC 434
              ||||  ||||||||||||||  ||||  ||||||||||||  ||||||||||||| ||||||
Db        243 CCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTCTGCACGAGTTAC 184

Qy        435 CTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAAAGAT-GGCAT 492
              |||  |||||  ||||||  |||  ||||||||||||||||||  ||||||  ||||||  ||| |
Db        183 CTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTAAAAGATGGGCGT 124

Qy        493 TTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||
Db        123 TTCCCCCAATGAAATACACAAGTAAACATTC 93
```

```
RESULT 13
AI169770/c
LOCUS       AI169770                468 bp    mRNA    linear   EST 20-JAN-1999
DEFINITION  EST215669 Normalized rat liver, Bento Soares Rattus sp. cDNA clone
            RLIAT07 3' end, mRNA sequence.
ACCESSION   AI169770
VERSION     AI169770.1  GI:3709810
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished
COMMENT     Other_ESTs: TC50779
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
```

```
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):2027570"
                     /db_xref="taxon:10118"
                     /clone="RLIAT07"
                     /clone_lib="Normalized rat liver, Bento Soares"
                     /note="Organ: liver; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT       85 a    115 c    119 g    149 t
ORIGIN

  Query Match             59.1%;  Score 309.2;  DB 9;  Length 468;
  Best Local Similarity   81.8%;  Pred. No. 7.2e-67;
  Matches  383;  Conservative    0;  Mismatches   78;  Indels    7;  Gaps    2;

Qy          63 GGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGAC 122
               ||||||||| |||||||||||||||| || |||||||||| |||||||||||| |||||
Db         468 GGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGAC 409

Qy         123 AGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
               ||||| |||||||||||| |||| |||||||||||||||||||||| ||||||||||||
Db         408 GGGCATTGTGGATGAGTGTTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349

Qy         183 TGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACAT 242
               ||| || || |||||  ||||| |||| || ||| |||| |||||||||||||| |||||
Db         348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACAT 289

Qy         243 GCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAG 302
               |||||||||||||||||  ||||| | ||| ||  ||||||||| ||||   || |||||
Db         288 GCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 229

Qy         303 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACA 362
               |||||||||||||||| |||||||||||||||||| ||||||||||||||| |||||
Db         228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 169

Qy         363 GGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 422
               | |||||||| || ||| | |||||    | || | || | ||||||| || ||||||||
Db         168 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109

Qy         423 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCAC 476
                       |    |||||| |||| ||| ||||      || ||| ||||  ||  |
Db         108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49

Qy         477 ATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               |||||| |||| |||||||||| ||||||||||||||||||||||||
Db          48 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 1


RESULT 14
AA542914/c
LOCUS       AA542914                498 bp    mRNA    linear   EST 19-AUG-1997
```

```
DEFINITION  ni98c10.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984882 3'
            similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AA542914
VERSION     AA542914.1  GI:2291394
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 498)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 603   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 412.
FEATURES             Location/Qualifiers
     source          1. .498
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:984882"
                     /sex="male"
                     /tissue_type="normal prostate"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr21"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is not normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      105 a    135 c    123 g    135 t
ORIGIN
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  Query Match             58.3%;  Score 305;  DB 9;  Length 498;
  Best Local Similarity   83.5%;  Pred. No. 8.2e-66;
  Matches  440;  Conservative    0;  Mismatches   30;  Indels   57;  Gaps    6;

Qy          1 GGACCGGAGACGCTCTGCGGTGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 59
              ||||||||||   | ||||| || ||||||||||||||||||||||||||||||||||||
Db        476 GGACCGGAGAACTTTTGCGGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417
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Qy         60 CAGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCA 119
              ||||||| |||||||||||||||||||| || ||||||||||||||||||| |||||
Db        416 CAGGGGC-TTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 358

Qy        120 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTA 179
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        357 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 298

Qy        180 CTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGA 239
               || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        297 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 238

Qy        240 CATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAG 299
              ||||||||||| |||
Db        237 CATGCCCAAGACCCAG---------------------------------------------- 222

Qy        300 GAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACT 359
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        221 --------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACT 170

Qy        360 ACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTT 419
              |||||||||||||||||||| |||||||||||||  |||| |||||||||||| |||||
Db        169 ACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTT 110

Qy        420 GCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACA 477
              ||||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| |||
Db        109 GCTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACA 50

Qy        478 TTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||| |||||| ||| ||||||||||||||||||||||||||||||||
Db         49 TTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 3
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RESULT 15
AI604642
LOCUS       AI604642                882 bp    mRNA    linear   EST 21-APR-1999
DEFINITION  vm43d08.y1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
            clone IMAGE:1001007 5' similar to gb:M11568 INSULIN-LIKE GROWTH
            FACTOR IB PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI604642
VERSION     AI604642.1  GI:4613809
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
```

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            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:565223
            This read is a RESEQUENCE of a previously sequenced mouse clone
            This read has been verified (found to hit its original self in the
            correct orientation)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 361.
FEATURES             Location/Qualifiers
     source          1. .882
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1001007"
                     /tissue_type="diaphragm"
                     /dev_stage="adult"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse diaphragm (#937303)"
                     /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA,
                     prepared from diaphragm muscle.  Primer: Oligo dT. Average
                     insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT      236 a    226 c    183 g    223 t     14 others
ORIGIN

  Query Match             57.2%;  Score 299;  DB 9;  Length 882;
  Best Local Similarity   77.2%;  Pred. No. 3e-64;
  Matches  393;  Conservative    0;  Mismatches  109;  Indels    7;  Gaps    3;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||| ||||||||||||||||||||||||||
Db        377 GGACCAGAGACCCTTTGCGGNGCTGAGCTGNTGGATGCTCTTCAGTTCGTGTGTGGACCG 436

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||| || |||||||||| |  ||||||||||||
Db        437 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGAGGGCACCTCAG 496

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||| ||| ||||||||||||
Db        497 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGANGAGACTGGAGATGTAC 556

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  || | |||||||||||  |||||||||||||||||| |||
Db        557 TGTGCCCCACTGAAGCCTACANAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 616

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||   ||||||||||||  | |   | ||| ||  |  ||||||| ||||  |   |||
Db        617 ATGCNNCAGACTCAGAAGTCCCCGTNCCTATCGACNNAACAGAAAACGAAGCTTGCAAGG 676

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                 ||| |||| |||||||||| ||||||| || |||| |||||| |||||||||  |||
```

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Db        677 GAGAGGGAAGGGAGTACATTTGAGGAACACANGTNGAGGAAGTGCANGAAACAAGACCTA 736

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |  |||||| || || |||||  |    | | ||||   ||   ||||    || ||||||
Db        737 CCAGATGTANGAGGAGCCTTC--AACCGAGCAGAAATGCACATCACCCGNAGATCCTTTG 794

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAA----AAAATAAGTTTGATCAC 476
              ||       || || ||| |||||| | |  ||   ||||    || |  |  || |  |
Db        795 CT-GCTTGAGCTAACTGCAAACATCGAACCACTTACCAATTACAATAATAAGTTCAATAA 853

Qy        477 ATTTCAAAGATGGCATTTCCCCCAATGAA 505
                | |||||||||||||||||||| ||||
Db        854 CATACAAAGATGGCATTTCCCCCATTGAA 882
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Search completed: December 13, 2003, 07:29:51
Job time : 1704.81 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20 ; Search time 2336.77 Seconds
(without alignments)
9156.102 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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8: gb_pl:*
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14: gb_vi:*
15: em_ba:*
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17: em_hum:*
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20: em_om:*
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35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	100.0	523	6	AX147746	AX147746 Sequence
2	523	100.0	523	6	AX300783	AX300783 Sequence
3	467.4	89.4	517	6	AX147742	AX147742 Sequence
4	467.4	89.4	517	6	AX300779	AX300779 Sequence
5	409	78.2	471	6	AX147754	AX147754 Sequence
6	409	78.2	471	6	AX300791	AX300791 Sequence
7	364.8	69.8	1536	10	BC012409	BC012409 Mus muscu
8	361.6	69.1	798	10	RNIGFI2	X06108 Rat mRNA (c
9	361.6	69.1	958	10	RNIGFI1	X06107 Rat mRNA (c
10	358.4	68.5	710	10	RATIGFIA	M15480 Rat insulin
11	356.8	68.2	539	6	AX147744	AX147744 Sequence
12	356.8	68.2	539	6	AX300781	AX300781 Sequence
13	349.4	66.8	651	10	MMIGFIBR	X04482 Mouse mRNA
14	336	64.2	432	4	AF022961	AF022961 Oryctolag
15	334.4	63.9	7260	6	AX375028	AX375028 Sequence
16	334.4	63.9	7260	6	AX411095	AX411095 Sequence
17	334.4	63.9	7260	9	HSIGFACI	X57025 Human IGF-I
18	332.8	63.6	666	6	A29119	A29119 H.sapiens I
19	332.8	63.6	725	9	HSIGFI	X00173 Homo sapien
20	332.8	63.6	728	9	HUMGFII	M29644 Human insul
21	332.4	63.6	616	9	HSIGF1A	X56773 H.sapiens m
22	331.2	63.3	620	6	I08370	I08370 Sequence 2
23	331.2	63.3	1076	9	HUMIGFI	M27544 Human insul
24	316.8	60.6	444	9	HSU40870	U40870 Human alter
25	293.8	56.2	532	4	SSILGF1M	X17492 Porcine mRN
26	293.8	56.2	567	4	PIGGFIIA	M31175 Pig insulin
27	286.2	54.7	888	4	ECU85272	U85272 Equus cabal
28	281.8	53.9	978	4	GOTIGFI	D11378 Goat mRNA f
29	281.8	53.9	978	6	E05279	E05279 DNA encodin
30	280.2	53.6	1284	4	BTILGF1A	X15726 Bovine mRNA
31	275.4	52.7	747	4	SHPIGFIA6	M31735 Sheep insul
32	275.4	52.7	790	4	SHPIGFIA21	M31734 Sheep insul
33	275.4	52.7	1015	4	SHPIGFIA46	M31736 Sheep insul

34	275.4	52.7	1107	4	SHPIGFIA1	M30653 Sheep insul
35	275.2	52.6	730	9	HSIGF1B	X56774 H.sapiens m
36	275.2	52.6	1094	9	HUMGFIB	M11568 Human insul
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38	275.2	52.6	1136	6	I08009	I08009 Sequence 3
39	274.6	52.5	3599	6	BD063790	BD063790 Insulin-l
40	274.6	52.5	3599	6	BD069041	BD069041 Treatment
41	274.6	52.5	3600	6	BD063789	BD063789 Insulin-l
42	274.6	52.5	3600	6	BD069040	BD069040 Treatment
43	273.6	52.3	612	9	HUMIGFIB	M37484 Human insul
44	271.6	51.9	696	10	MMIGFIAR	X04480 Mouse mRNA
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ALIGNMENTS

RESULT 1
AX147746
LOCUS AX147746 523 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 5 from Patent WO0136483.
ACCESSION AX147746
VERSION AX147746.1 GI:14346791
KEYWORDS .
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1
AUTHORS Goldspink,G.R. and Johnson,I.R.
TITLE Use of the insulin-like-growth factor i isoform mgf for the
treatment of neurological disorders
JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;
University College London (GB)
FEATURES Location/Qualifiers
source 1. .523
/organism="Oryctolagus cuniculus"
/mol_type="genomic DNA"
/db_xref="taxon:9986"
CDS <1. .336
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC41177.1"
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BASE COUNT 154 a 129 c 142 g 98 t
ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 9.5e-150;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 2
AX300783
LOCUS       AX300783                 523 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 5 from Patent WO0185781.
ACCESSION   AX300783
VERSION     AX300783.1  GI:17382064
KEYWORDS    .
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 5 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
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                     KGSTFEEHK"
BASE COUNT      154 a    129 c    142 g     98 t
ORIGIN
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Query Match 100.0%; Score 523; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 9.5e-150;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 3
AX147742
LOCUS       AX147742                517 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 1 from Patent WO0136483.
ACCESSION   AX147742
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VERSION     AX147742.1  GI:14346787
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
  JOURNAL   Patent: WO 0136483-A 1 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             <1. .333
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41175.1"
                     /db_xref="GI:14346788"
                     /db_xref="REMTREMBL:CAC41175"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
                     GSTFEEHK"
BASE COUNT      150 a    130 c    139 g     98 t
ORIGIN
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Query Match 89.4%; Score 467.4; DB 6; Length 517;
Best Local Similarity 96.2%; Pred. No. 1.3e-132;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||||||||||||| |||||||||||||||| | |||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
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Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
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Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 4
AX300779
LOCUS       AX300779                 517 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1 from Patent WO0185781.
ACCESSION   AX300779
VERSION     AX300779.1  GI:17382060
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 1 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             <1. .333
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13040.1"
                     /db_xref="GI:17382061"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
                     GSTFEEHK"
BASE COUNT      150 a    130 c    139 g     98 t
ORIGIN

  Query Match             89.4%;  Score 467.4;  DB 6;  Length 517;
  Best Local Similarity   96.2%;  Pred. No. 1.3e-132;
  Matches  501;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||||||||||||| |||||||||||||||| | |||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
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RESULT 5
AX147754
LOCUS       AX147754                 471 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 13 from Patent WO0136483.
ACCESSION   AX147754
VERSION     AX147754.1  GI:14348552
KEYWORDS    .
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
  JOURNAL   Patent: WO 0136483-A 13 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Oryctolagus cuniculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9986"
     CDS             <1. .318
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41264.1"
                     /db_xref="GI:14348553"
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                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
                     YRM"
BASE COUNT      132 a    118 c    131 g     90 t
ORIGIN

  Query Match             78.2%;  Score 409;  DB 6;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 1.3e-114;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 6
AX300791
LOCUS       AX300791                 471 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 13 from Patent WO0185781.
ACCESSION   AX300791
VERSION     AX300791.1  GI:17382072
KEYWORDS    .
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 13 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .471
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9986"
     CDS             <1. .318
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13045.1"
                     /db_xref="GI:17382073"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
                     YRM"
BASE COUNT      132 a    118 c    131 g     90 t
ORIGIN

  Query Match             78.2%;  Score 409;  DB 6;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 1.3e-114;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 7
BC012409
LOCUS       BC012409                1536 bp    mRNA    linear   ROD 16-APR-2003
DEFINITION  Mus musculus insulin-like growth factor 1, mRNA (cDNA clone
            MGC:18617 IMAGE:4194295), complete cds.
ACCESSION   BC012409
VERSION     BC012409.1  GI:15214568
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1536)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1536)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
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Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 24 Row: k Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754307.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="MGC:18617 IMAGE:4194295"
                     /tissue_type="Liver, normal. 5 month old male mouse."
                     /clone_lib="NCI_CGAP_Li9"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .1536
                     /gene="Igf1"
                     /db_xref="LocusID:16000"
                     /db_xref="MGI:96432"
     CDS             28. .429
                     /codon_start=1
                     /product="insulin-like growth factor 1"
                     /protein_id="AAH12409.1"
                     /db_xref="GI:15214569"
                     /db_xref="LocusID:16000"
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                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD
                     MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
BASE COUNT      485 a    324 c    303 g    424 t
ORIGIN
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  Query Match             69.8%;  Score 364.8;  DB 10;  Length 1536;
  Best Local Similarity   83.2%;  Pred. No. 6.6e-101;
  Matches  441;  Conservative    0;  Mismatches   82;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db         94 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 153

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        154 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 213

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| ||||||||||||||||||||||||| ||||||||||||
Db        214 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 273

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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                |||||  ||  ||  |||||  ||||  ||||||||||  ||||||||||||||||||| |||
Db        274 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 333

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
                |||||||||||||||||  | | | | |||  ||  ||||||||||  ||||    ||  |||
Db        334 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 393

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                |||||||||||||||||||||||||||||||||||||||  ||||||||||||||  |||
Db        394 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 453

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
                |||  ||||||||  ||  |||  |   ||||   |  ||  |  ||   ||||||||||  ||||||
Db        454 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 513

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
                ||            |    ||||||  |  ||  |||  |||       ||  |||||||   ||
Db        514 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 573

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
                |||||  |||||||  ||||||||||||||||||||  ||||||||||||||
Db        574 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTC 623
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RESULT 8
RNIGFI2
LOCUS       RNIGFI2                   798 bp    mRNA    linear   ROD 12-SEP-1993
DEFINITION  Rat mRNA (clone IGF1AB2) for insulin-like growth factor I.
ACCESSION   X06108 M32339 Y00429
VERSION     X06108.1  GI:56426
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Sequence of Two Rat Insulin-like Growth Factor I mRNAs Differing
            Within the 5' Untranslated Region
  JOURNAL   Nucleic Acids Res. 15 (1987) In press
REFERENCE   2  (bases 1 to 798)
  AUTHORS   Rotwein,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1987) Rotwein P., Washington University, School
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
            63110, USA
COMMENT     Another IGF-I mRNA of rat liver differing in the 5' UT-region is
            described in <X06107>.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     misc_feature    1. .72
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                     /note="5' UT-region"
     CDS             73. .552
                     /note="IGF-I (AA 1-159)"
                     /codon_start=1
                     /protein_id="CAA29481.1"
                     /db_xref="GI:56427"
                     /translation="MGKISSLPTQLFKICLCDFLKIKIHIMSSSHLFYLALCLLTFTS
                     SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGIVDECCFRSCDL
                     RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     misc_feature    553. .798
                     /note="3' UT-region"
BASE COUNT      238 a    196 c    183 g    181 t
ORIGIN
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Query Match 69.1%; Score 361.6; DB 10; Length 798;
Best Local Similarity 82.8%; Pred. No. 5.8e-100;
Matches 439; Conservative 0; Mismatches 84; Indels 7; Gaps 2;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db        217 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 276

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| |||||||||||| |||
Db        277 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 336

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        337 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 396

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  ||||| |||| || ||| |||| ||||||||||||||| |||
Db        397 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 456

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  ||||| | ||| ||  ||||||||| ||||   || |||
Db        457 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 516

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| ||||||||||||||| |||
Db        517 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 576

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||     | || | || | ||||||| || ||||||
Db        577 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 636

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        637 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 696

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| |||||||||||||||||||||||
Db        697 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 746
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RESULT 9
RNIGFI1

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LOCUS       RNIGFI1                   958 bp    mRNA    linear   ROD 12-SEP-1993
DEFINITION  Rat mRNA (clone IGF1AB1) for insulin-like growth factor I.
ACCESSION   X06107 M32260 Y00429
VERSION     X06107.1  GI:56424
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Sequence of two rat insulin-like growth factor I mRNAs differing
            within the 5' untranslated region
  JOURNAL   Nucleic Acids Res. 15 (17), 7196 (1987)
  MEDLINE   88015572
   PUBMED   3658684
REFERENCE   2  (bases 1 to 958)
  AUTHORS   Rotwein,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1987) Rotwein P., Washington University, School
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
            63110, USA
COMMENT     Another IGF-I mRNA of rat liver differing in the 5' UT-region is
            described in <X06108>.
FEATURES             Location/Qualifiers
     source          1. .958
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Srpague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     misc_feature    1. .258
                     /note="5' UT-region"
     CDS             259. .738
                     /note="IGF-I (AA 1-159)"
                     /codon_start=1
                     /protein_id="CAA29480.1"
                     /db_xref="GI:56425"
                     /db_xref="SWISS-PROT:P08024"
                     /translation="MGKISSLPTQLFKICLCDFLKIKIHIMSSSHLFYLALCLLTFTS
                     SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGIVDECCFRSCDL
                     RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     misc_feature    736. .958
                     /note="3' UT-region"
BASE COUNT      260 a    246 c    209 g    243 t
ORIGIN
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  Query Match             69.1%;  Score 361.6;  DB 10;  Length 958;
  Best Local Similarity   82.8%;  Pred. No. 6e-100;
  Matches  439;  Conservative    0;  Mismatches   84;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db        403 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 462

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db        463 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 522

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db        523 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 582

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
Db        583 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 642

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db        643 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 702

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db        703 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 762

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Db        763 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 822

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
Db        823 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 882

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Db        883 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 932
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RESULT 10
RATIGFIA
LOCUS       RATIGFIA                  710 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION   M15480
VERSION     M15480.1  GI:204749
KEYWORDS    growth factor; insulin-like growth factor.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and
            LeRoith,D.
  TITLE     Molecular cloning of rat insulin-like growth factor I complementary
            deoxyribonucleic acids: differential messenger ribonucleic acid
            processing and regulation by growth hormone in extrahepatic tissues
  JOURNAL   Mol. Endocrinol. 1 (3), 243-248 (1987)
  MEDLINE   88288198
   PUBMED   3453891
COMMENT     Original source text: Rat (Sprague-Dawley) adult liver cDNA to
            mRNA, clone pRIGF-1-42.
            Draft entry and computer-readable copy of sequence in [Mol.
            Endocrinol. (1987) In press] kindly
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            provided by S.R.Lasky, 16-MAR-1987.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
     CDS             106. .507
                     /note="insulin-like growth factor precursor"
                     /codon_start=1
                     /protein_id="AAA41385.1"
                     /db_xref="GI:204750"
                     /translation="MSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTD
                     MPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     sig_peptide     106. .171
                     /note="insulin-like growth factor signal peptide"
     mat_peptide     172. .258
                     /product="insulin-like growth factor B peptide"
     mat_peptide     259. .294
                     /product="insulin-like growth factor C peptide"
     mat_peptide     295. .357
                     /product="insulin-like growth factor A peptide"
     mat_peptide     358. .381
                     /product="insulin-like growth factor D peptide"
     mat_peptide     382. .504
                     /product="insulin-like growth factor E peptide"
BASE COUNT      202 a    191 c    172 g    145 t
ORIGIN      1 bp upstream of EcoRI site.

  Query Match             68.5%;  Score 358.4;  DB 10;  Length 710;
  Best Local Similarity   82.5%;  Pred. No. 5.5e-99;
  Matches  437;  Conservative    0;  Mismatches   86;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db        172 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 231

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| |||||||||||| |||
Db        232 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 291

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        292 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 351

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| ||||||||||||| |||
Db        352 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 411

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        412 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 471

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        472 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 531
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Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        532 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 591

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        592 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 651

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        652 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 701


RESULT 11
AX147744
LOCUS       AX147744                 539 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 3 from Patent WO0136483.
ACCESSION   AX147744
VERSION     AX147744.1  GI:14346789
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
  JOURNAL   Patent: WO 0136483-A 3 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
     CDS             <1. .336
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41176.1"
                     /db_xref="GI:14346790"
                     /db_xref="REMTREMBL:CAC41176"
                     /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                     DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRR
                     KGSTLEEHK"
BASE COUNT      161 a    136 c    139 g    103 t
ORIGIN

  Query Match             68.2%;  Score 356.8;  DB 6;  Length 539;
  Best Local Similarity   82.3%;  Pred. No. 1.6e-98;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||||||| ||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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                ||||||||||| |||||||||||||||  || |||||||||| |||||||||||| |||
Db          61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy         121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
                || ||||| |||||||||||| |||||||||||||||||||||||||||||||||||||
Db         121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy         181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
                ||||  | |  ||||||  ||||| |||| || ||| |||| |||||||||||||| |||
Db         181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy         241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
                |||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db         241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy         301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db         301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy         361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
                ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db         361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy         421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
                ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db         421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy         475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
                ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db         481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
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RESULT 12
AX300781
LOCUS       AX300781                 539 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 3 from Patent WO0185781.
ACCESSION   AX300781
VERSION     AX300781.1  GI:17382062
KEYWORDS    .
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 3 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Rattus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10118"
     CDS             <1. .336
                     /note="unnamed protein product"
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                     /codon_start=1
                     /protein_id="CAD13041.1"
                     /db_xref="GI:17382063"
                     /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                     DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRR
                     KGSTLEEHK"
BASE COUNT      161 a    136 c    139 g    103 t
ORIGIN
```

Query Match 68.2%; Score 356.8; DB 6; Length 539;
Best Local Similarity 82.3%; Pred. No. 1.6e-98;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| ||||||||||||||||  || |||||||||| |||||||||||  |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| ||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| ||||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
```

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RESULT 13
MMIGFIBR
LOCUS       MMIGFIBR                  651 bp    mRNA    linear   ROD 21-MAR-1995
DEFINITION  Mouse mRNA for preproinsulin-like growth factor IB.
ACCESSION   X04482
VERSION     X04482.1  GI:51806
KEYWORDS    growth factor; insulin-like growth factor IB; preproinsulin-like
```

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            growth factor IB; signal peptide.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Bell,G.I., Stempien,M.M., Fong,N.M. and Rall,L.B.
  TITLE     Sequences of liver cDNAs encoding two different mouse insulin-like
            growth factor I precursors
  JOURNAL   Nucleic Acids Res. 14 (20), 7873-7882 (1986)
  MEDLINE   87040760
   PUBMED   3774549
COMMENT     The sequence is identical to the preproIGF-IA sequence (X04480)
            except for the presence of a 52 bp insertion following codon 86
            (position 397 to 448), caused by alternative RNA splicing. The B
            domain of IGF comprises residues 1-29 (position 139-225), the C
            domain residues 30-41 (position 226-261), the A domain residues
            42-62 (position 262-324) and the D domain residues 63-70 (position
            325-348).
FEATURES             Location/Qualifiers
     source          1. .651
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="Balb/c"
                     /db_xref="taxon:10090"
                     /clone="migfl-4"
                     /tissue_type="liver"
     misc_feature    43. .45
                     /note="pot. translation start"
     CDS             73. .474
                     /note="prepro IGF-IB (aa -22 to 111)"
                     /codon_start=1
                     /protein_id="CAA28170.1"
                     /db_xref="GI:51807"
                     /db_xref="MGI:96432"
                     /db_xref="SWISS-PROT:P05018"
                     /translation="MSSSHLFYLALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD
                     MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
     sig_peptide     73. .138
                     /note="signal peptide (aa -22 to -1)"
     mat_peptide     139. .348
                     /product="mature IGF-IB (aa 1-70)"
     misc_feature    349. .471
                     /note="COOH-terminal peptide (E domain) (aa 71 to 111)"
     polyA_site      651
                     /note="polyA site"
BASE COUNT      193 a    185 c    149 g    124 t
ORIGIN

  Query Match             66.8%;  Score 349.4;  DB 10;  Length 651;
  Best Local Similarity   82.8%;  Pred. No. 3.2e-96;
  Matches  425;  Conservative    0;  Mismatches   81;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198
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Qy          61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
               ||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db         199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy         121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
               |||||||| |||||||||| ||||||||||||||||||||||||| ||||||||||||
Db         259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy         181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
               ||||| || || |||||  |||| ||||||||||  ||||||||||||||||||| |||
Db         319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378

Qy         241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
               ||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db         379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy         301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
               |||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db         439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy         361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
               ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db         499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy         421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
               ||           |    |||||| | || |||  |||      || |||||||   ||
Db         559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy         475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
               ||||| ||||||| ||||||||||||||||||
Db         619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651
```

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RESULT 14
AF022961
LOCUS       AF022961                 432 bp    mRNA    linear   MAM 14-OCT-1997
DEFINITION  Oryctolagus cuniculus insulin-like growth factor IB (IGF-IB) mRNA,
            complete cds.
ACCESSION   AF022961
VERSION     AF022961.1  GI:2522201
KEYWORDS    .
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Flekna,G., Brem,G. and Mueller,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-1997) Institute of Animal Breeding and Genetics,
            Veterinary University of Vienna, Veterinaerplatz 1, Vienna A-1210,
            Austria
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="Oryctolagus cuniculus"
                     /mol_type="mRNA"
                     /strain="ZIKA hybrid strain"
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                     /db_xref="taxon:9986"
                     /cell_type="primary liver cells"
                     /tissue_type="liver"
     gene            1. .432
                     /gene="IGF-IB"
     CDS             1. .432
                     /gene="IGF-IB"
                     /codon_start=1
                     /product="insulin-like growth factor IB"
                     /protein_id="AAB80950.1"
                     /db_xref="GI:2522202"
                     /translation="MITPTVKMRILSSSHLFYLALCLLTFTSSATAGPETLCGAELVD
                     ALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPAKAA
                     RSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRRKGSTFEEHK"
BASE COUNT      105 a    126 c    115 g     86 t
ORIGIN

  Query Match             64.2%;  Score 336;  DB 4;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-92;
  Matches  336;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 156

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 216

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 276

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 336

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 396

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG 336
              ||||||||||||||||||||||||||||||||||||
Db        397 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG 432


RESULT 15
AX375028
LOCUS       AX375028               7260 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 31 from Patent WO0210436.
ACCESSION   AX375028
VERSION     AX375028.1  GI:19169860
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Baak,J. and Mutter,G.L.
  TITLE     Prognostic classification of breast cancer
  JOURNAL   Patent: WO 0210436-A 31 07-FEB-2002;
            THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)
FEATURES             Location/Qualifiers
     source          1. .7260
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT     2330 a   1415 c   1240 g   2275 t
ORIGIN

  Query Match             63.9%;  Score 334.4;  DB 6;  Length 7260;
  Best Local Similarity   84.6%;  Pred. No. 2e-91;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||| || ||| |||| ||||| |||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| ||| |||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


Search completed: December 13, 2003, 09:27:34
Job time : 2336.77 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 02:35:18 ; Search time 209.995 Seconds
(without alignments)
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Perfect score: 523
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	100.0	523	22	AAD06400	Rabbit IGF-I isofo
2	523	100.0	523	24	AAS16879	Rabbit mechano-gro
3	523	100.0	553	18	AAT84893	Rabbit insulin lik
4	467.4	89.4	517	22	AAD06398	Human IGF-I isofor
5	467.4	89.4	517	24	AAS16877	Human mechano-grow
6	409	78.2	471	22	AAD06405	Rabbit liver-type
7	409	78.2	471	24	AAS16884	Rabbit insulin-lik
8	356.8	68.2	539	22	AAD06399	Rat IGF-I isoform
9	356.8	68.2	539	24	AAS16878	Rat mechano-growth
10	349.4	66.8	651	25	ABV76185	Mouse insulin-like
11	334.4	63.9	818	8	AAN70436	Sequence encoding
12	334.4	63.9	7260	24	ABT11091	Human breast cance
13	334.4	63.9	7260	24	ABK84583	Human cDNA differe
14	334.4	63.9	7260	24	ABN97244	Gene #3742 used to
15	334.4	63.9	7260	24	ABK64812	Human benign prost
16	334.4	63.9	7260	24	ABK35504	Human endometrial
17	334.4	63.9	7260	24	ABK35561	Gene IGF1 differen
18	332.8	63.6	777	18	AAT84894	Human insulin like
19	331.2	63.3	622	7	AAN60490	Human prepro-somat
20	281.8	53.9	978	14	AAQ47804	Sequence encoding
21	275.2	52.6	1136	8	AAN70435	Sequence encoding
22	274.6	52.5	3599	19	AAV50428	Plasmid pIG0552 lo
23	274.6	52.5	3599	19	AAV40796	Actual sequence of
24	274.6	52.5	3600	19	AAV50427	Plasmid pIG0552 up
25	274.6	52.5	3600	19	AAV40795	Expected sequence
26	274.6	52.5	5707	20	AAX88055	Plasmid pIG0335 DN
27	274.6	52.5	6345	20	AAX88054	Plasmid pIG0100A D
28	273.6	52.3	612	22	AAS14695	Human cDNA encodin
29	273.6	52.3	612	25	ABZ83309	Toxicologically re
30	266.8	51.0	1052	20	AAX27498	Rat liver form of
31	262	50.1	487	22	AAD06404	Rat liver-type IGF
32	262	50.1	487	24	AAS16883	Rat insulin-like g
33	250	47.8	671	24	ABT09479	Phase-1 Rat CT gen
34	237.6	45.4	317	24	AAS16882	Human insulin-like
35	237.6	45.4	318	22	AAD06403	Human liver-type I
36	237.6	45.4	462	19	AAV50426	Human IGF-1 encodi
37	237.6	45.4	462	19	AAV40794	Human IGF-I coding
38	237.6	45.4	462	24	ABZ35734	Human IGF1 polynuc
39	237.6	45.4	462	24	ABX09977	Human IGF1 DNA fra
40	237.6	45.4	462	24	ABV78158	Human IGF1 DNA SEQ
41	237.6	45.4	462	24	ABL91699	Human polynucleoti
42	209	40.0	286	25	ABV76186	Mouse insulin-like
43	193	36.9	210	24	AAD45568	Human insulin-like
44	193	36.9	210	24	AAD44955	Human insulin grow
45	193	36.9	210	24	ABA03146	Native mature IGF-

ALIGNMENTS

RESULT 1
AAD06400
ID   AAD06400 standard; cDNA; 523 BP.
XX
AC   AAD06400;
XX
DT   10-AUG-2001 (first entry)
XX
DE   Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW   Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW   nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW   sex-linked muscular dystrophy; peripheral neuropathy;
KW   Alzheimer's disease; Parkinson's disease; ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..336
FT   /*tag= a
FT   /product= "Mechano-growth factor (MGF)"
FT   /note= "This region comprises exons 3-6. The CDS does
FT   not include start codon"
FT   /partial
XX
PN   WO200136483-A1.
XX
PD   25-MAY-2001.
XX
PF   15-NOV-2000; 2000WO-GB04354.
XX
PR   15-NOV-1999;   99GB-0026968.
XX
PA   (UNLO) UNIV COLLEGE LONDON.
XX
PI   Goldspink G, Johnson I;
XX
DR   WPI; 2001-355620/37.
DR   P-PSDB; AAE02449.
XX
PT   Use of mechano-growth factor, an isoform of Insulin-like Growth
PT   Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT   medicament for the treatment of neurological disorder -
XX
PS   Claim 4; Page 53-54; 66pp; English.
XX
CC   The present invention relates to use of mechano-growth factor (MGF),
CC   an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC   medicament for the treatment of neurological disorder. The MGF is capable
CC   of reducing motoneurone loss by 20% or greater in response to nerve
CC   avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC   rescue. The MGF polynucleotide and polypeptide are useful in the
CC   manufacture of a medicament for the treatment of a neurological disorder,
CC   including a disorder of motoneurones and/or neurodegenerative disorder,

CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.
XX
SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 22; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.1e-144;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
```

RESULT 2

```
AAS16879
ID   AAS16879 standard; cDNA; 523 BP.
XX
AC   AAS16879;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Rabbit mechano-growth factor (MGF) cDNA.
XX
KW   Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW   nerve avulsion.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..336
FT                   /*tag=  a
FT                   /product= "Rabbit MGF"
FT                   /partial
FT                   /note= "No start codon"
FT   exon            1..76
FT                   /*tag=  b
FT                   /number= 3
FT   exon            77..259
FT                   /*tag=  c
FT                   /number= 4
FT   exon            260..309
FT                   /*tag=  d
FT                   /number= 5
FT   exon            311..333
FT                   /*tag=  e
FT                   /number= 6
XX
PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G,  Terenghi G;
XX
DR   WPI; 2002-055585/07.
DR   P-PSDB; AAU10561.
XX
PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage  -
XX
PS   Disclosure; Fig 7; 65pp; English.
```

XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit MGF.
XX
SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 24; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.1e-144;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
```

RESULT 3
AAT84893
ID AAT84893 standard; cDNA; 553 BP.
XX
AC AAT84893;
XX
DT 14-APR-1998 (first entry)
XX
DE Rabbit insulin like growth factor 1 encoding cDNA.
XX
KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW heart; neuromuscular disease; primer; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key   Location/Qualifiers
FT CDS   1..366
FT   /*tag= a
FT   /product= "IGF-1"
XX
PN WO9733997-A1.
XX
PD 18-SEP-1997.
XX
PF 11-MAR-1997;   97WO-GB00658.
XX
PR 11-MAR-1996;   96GB-0005124.
XX
PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI Goldspink G;
XX
DR WPI; 1997-470877/43.
DR P-PSDB; AAW23301.
XX
PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases
XX
PS Disclosure; Fig 3; 33pp; English.
XX
CC A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial
CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes rabbit
CC IGF-1 used in the present specification.
XX
SQ Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

```
  Query Match             100.0%;  Score 523;  DB 18;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-144;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553


RESULT 4
AAD06398
ID   AAD06398 standard; cDNA; 517 BP.
XX
AC   AAD06398;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW   Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW   nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
```

KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= "Mechano-growth factor (MGF)"
FT /note= "This region comprises exons 3-6. The CDS does
FT not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-GB04354.
XX
PR 15-NOV-1999; 99GB-0026968.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Goldspink G, Johnson I;
XX
DR WPI; 2001-355620/37.
DR P-PSDB; AAE02447.
XX
PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
PS Claim 4; Page 49-50; 66pp; English.
XX
CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.
XX
SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 22; Length 517;
Best Local Similarity 96.2%; Pred. No. 1.3e-127;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||||||||||||| |||||||||||||||| | |||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
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RESULT 5
AAS16877
ID AAS16877 standard; cDNA; 517 BP.
XX
AC AAS16877;
XX
DT 25-FEB-2002 (first entry)
XX
DE Human mechano-growth factor (MGF) cDNA.
XX
KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW nerve avulsion.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= "Human MGF"
FT /partial
FT /note= "No start codon"
FT exon 1..76
FT /*tag= b
FT /number= 3
FT exon 77..259
FT /*tag= c
FT /number= 4
FT exon 260..307
FT /*tag= d
FT /number= 5
FT exon 308..330
FT /*tag= e
FT /number= 6
XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI Goldspink G, Terenghi G;
XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10559.
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -
XX
PS Claim 11; Fig 5; 65pp; English.
XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the human MGF.
XX

```
SQ   Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

  Query Match             89.4%;  Score 467.4;  DB 24;  Length 517;
  Best Local Similarity   96.2%;  Pred. No. 1.3e-127;
  Matches  501;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||||||||||||| |||||||||||||||| | |||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 6
AAD06405
ID   AAD06405 standard; cDNA; 471 BP.
XX
AC   AAD06405;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
XX
KW   Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
```

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..318
FT /*tag= a
FT /product= "Liver-type IGF-I isoform (L.IGF-I)"
FT /transl_except= (pos:7..9, aa:Gln)
FT /transl_except= (pos:25..27, aa:Gln)
FT /note= "These translation exceptions occur while decoding
FT the alternative version of the protein (AAE02456).
FT The CDS comprises exons 3, 4 and 6 and
FT does not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-GB04354.
XX
PR 15-NOV-1999; 99GB-0026968.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Goldspink G, Johnson I;
XX
DR WPI; 2001-355620/37.
DR P-PSDB; AAE02452, AAE02456.
XX
PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
PS Disclosure; Page 59-60; 66pp; English.
XX
CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
CC The L.IGF-I protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4 and 6.

```
XX
SQ   Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

  Query Match             78.2%;  Score 409;  DB 22;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 2e-110;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 7
AAS16884
ID   AAS16884 standard; cDNA; 471 BP.
XX
AC   AAS16884;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.
XX
KW   Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
```

KW nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..318
FT /*tag= a
FT /product= "Rabbit L.IGF-I"
FT /partial
FT /note= "No start codon"
FT exon 1..75
FT /*tag= b
FT /number= exon 3
FT exon 76..258
FT /*tag= c
FT /number= exon 4
FT exon 259..315
FT /*tag= d
FT /number= exon 6
XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI Goldspink G, Terenghi G;
XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10564.
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -
XX
PS Disclosure; Fig 10; 65pp; English.
XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like
CC growth factor I liver-type isoform (L.IGF-I) used in experiments on

```
CC   motoneuron loss.
XX
SQ   Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

  Query Match             78.2%;  Score 409;  DB 24;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 2e-110;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 8
AAD06399
ID   AAD06399 standard; cDNA; 539 BP.
XX
AC   AAD06399;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Rat IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW   Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
```

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..336
FT /*tag= a
FT /product= "Mechano-growth factor (MGF)"
FT /note= "This region comprises exons 3-6. The CDS does
FT not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-GB04354.
XX
PR 15-NOV-1999; 99GB-0026968.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Goldspink G, Johnson I;
XX
DR WPI; 2001-355620/37.
DR P-PSDB; AAE02448.
XX
PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
PS Claim 4; Page 51-52; 66pp; English.
XX
CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.

```
XX
SQ   Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

  Query Match             68.2%;  Score 356.8;  DB 22;  Length 539;
  Best Local Similarity   82.3%;  Pred. No. 5.1e-95;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||||||| ||||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| ||||||||||||||||  || |||||||||| |||||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  |||||| ||||| |||| || ||| |||| |||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  ||||||||| ||||   || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530


RESULT 9
AAS16878
ID   AAS16878 standard; cDNA; 539 BP.
XX
AC   AAS16878;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Rat mechano-growth factor (MGF) cDNA.
XX
KW   Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
```

KW nerve avulsion.
XX
OS Rattus sp.
XX
FH Key   Location/Qualifiers
FT CDS   1..336
FT   /*tag= a
FT   /product= "Rat MGF"
FT   /partial
FT   /note= "No start codon"
FT exon   1..75
FT   /*tag= b
FT   /number= exon 3
FT exon   76..258
FT   /*tag= c
FT   /number= exon 4
FT exon   259..309
FT   /*tag= d
FT   /number= exon 5
FT exon   310..333
FT   /*tag= e
FT   /number= exon 6
XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI Goldspink G, Terenghi G;
XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10560.
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -
XX
PS Disclosure; Fig 6; 65pp; English.
XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These

```
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the rat MGF.
XX
SQ   Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

  Query Match             68.2%;  Score 356.8;  DB 24;  Length 539;
  Best Local Similarity   82.3%;  Pred. No. 5.1e-95;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||||||| ||||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| ||||||||||||||||  || |||||||||| |||||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| |||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530


RESULT 10
ABV76185
ID   ABV76185 standard; cDNA; 651 BP.
XX
AC   ABV76185;
XX
DT   07-MAR-2003  (first entry)
XX
DE   Mouse insulin-like growth factor IB cDNA.
XX
KW   Insulin-like growth factor IB; IGF-IB; mouse; mRNA; assay;
```

KW nucleic acid detection; gene; ss.
XX
OS Mus musculus.
XX
FH Key   Location/Qualifiers
FT CDS   73..474
FT   /*tag= a
FT   /product= "IGF-IB"
XX
PN WO200297390-A2.
XX
PD 05-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-SE01056.
XX
PR 01-JUN-2001; 2001SE-0001934.
XX
PA (BIOV-) BIOVITRUM AB.
XX
PI Parrow V, Rosengren L;
XX
DR WPI; 2003-129529/12.
XX
PT Quantitating a target nucleic acid in a sample comprises immobilizing,
PT on a solid support, a sample comprising a target nucleic acid, and
PT detecting and quantitating signals generated from the antisense and
PT sense probes -
XX
PS Example 1; Page 16-17; 18pp; English.
XX
CC The present sequence is that of cDNA encoding murine insulin-like
CC growth factor 1B (IGF-IB). The cDNA was used in an example of the
CC method of the invention to generate probes for determination of
CC IGF-IB RNA. The method comprises a quantitative hybridisation
CC assay for analysis of mRNA in a target nucleic acid (TNA) sample.
CC It involves: (i) immobilising the TNA sample on a solid support;
CC (ii) contacting a labelled antisense probe to a first portion of the
CC TNA, and a labelled sense probe to a second portion of the TNA;
CC (iii) detecting and quantitating the signals generated from the
CC hybridised probes; and (iv) determining the value represented by
CC the antisense probe signal minus the sense probe signal, the value
CC being proportional to the amount of mRNA in the TNA sample. In an
CC example of the method, a cDNA clone containing 60 nucleotides from
CC exon 2 and 179 nucleotides from exon 3 of the mouse IGF-IB gene was
CC cloned into pGEN-4Z vector. Linearisation of the plasmid with
CC EcoRI allowed transcription of a 250-nucleotide antisense probe
CC using T7 polymerase. Linearisation with HindIII allowed
CC transcription of a sense probe of similar length using SP6
CC polymerase (see ABV76186). The probes were purified and used to
CC determine IGF-I RNA in mouse hepatocytes and also in rat hepatocytes.
XX
SQ Sequence 651 BP; 193 A; 185 C; 149 G; 124 T; 0 other;

Query Match 66.8%; Score 349.4; DB 25; Length 651;
Best Local Similarity 82.8%; Pred. No. 8.3e-93;
Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||| ||||||||||||
Db        259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  |||||||||||||||||| |||
Db        319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| | || |||  |||      || |||||||   ||
Db        559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
              ||||| ||||||| ||||||||||||||||||
Db        619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651
```

```
RESULT 11
AAN70436
ID   AAN70436 standard; cDNA; 818 BP.
XX
AC   AAN70436;
XX
DT   25-MAR-2003  (updated)
DT   05-APR-1991  (first entry)
XX
DE   Sequence encoding insulin-like growth factor 1A (IGF-1A).
XX
KW   Growth promoter; lactation enhancer;  cell proliferation; ss.
XX
OS   Homo sapiens.
XX
PN   EP229750-A.
XX
PD   22-JUL-1987.
XX
PF   06-JAN-1987;   87EP-0870001.
```

XX
PR 20-NOV-1986; 86US-0929671.
PR 07-JAN-1986; 86US-0816662.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Krivi GG, Rotwein PS;
XX
DR WPI; 1987-200203/29.
XX
PT New pre-pro-insulin-like growth factor-1 protein - obtd. by
PT recombinant DNA procedures for use as growth promoters for
PT enhancing lactation, for stimulating cell proliferation etc.
XX
PS Example; Fig 5; 59pp; English.
XX
CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
CC amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
CC The radiolabeled 42 mer was then employed to screen for IGF-I
CC containing DNA sequences in a human liver cDNA library. Insulin-
CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
CC library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1
CC genomic gene was isolated and mapped. It encodes at least two
CC preproinsulin-like growth factor-1 proteins. An essentially pure
CC proproinsulin-like growth factor-1 protein comprising the sequence
CC of amino acids shown in Figure six is claimed (AAP70277).
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 63.9%; Score 334.4; DB 8; Length 818;
Best Local Similarity 84.6%; Pred. No. 2.4e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        263 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        383 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 442

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        443 ATGCCCAAGACCCAG---------------------------------------------- 457

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        458 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510
```

```
Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||||| ||||||||||||||  |||| |||||||||||| ||||||
Db        511 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 570

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  ||||||||||||||||| ||||
Db        571 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 630

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| |||||||||||||||||||||||||||||||
Db        631 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 676
```

RESULT 12
ABT11091
ID ABT11091 standard; cDNA; 7260 BP.
XX
AC ABT11091;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human breast cancer associated coding sequence SEQ ID NO: 1225.
XX
KW Human; breast specific gene; breast cancer; differential expression;
KW cytostatic; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200259271-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US02176.
XX
PR 25-JAN-2001; 2001US-263757P.
PR 25-APR-2001; 2001US-286090P.
PR 23-MAY-2001; 2001US-292517P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Orr MS, Nation M, Diggans JC, Zeng W;
XX
DR WPI; 2002-674803/72.
XX
PT Diagnosing breast cancer in a patient comprises detecting the level of
PT gene expression in cell or tissue samples, where a differential gene
PT expression is indicative of breast cancer -
XX
PS Claim 1; SEQ ID NO 1225; 260pp + Sequence Listing; English.
XX
CC The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABT09867-
CC ABT11112, where a differential expression of the genes indicates breast
CC cancer. The methods are useful in diagnosing, treating, detecting the
CC progression, and in monitoring treatment of breast cancer in patients.

```
CC   The methods are also useful as a screening tool for agents that modulate
CC   the onset or progression of breast cancer. The breast cancer genes may be
CC   used as diagnostic markers for the prediction or identification of the
CC   malignant state of breast tissue, for confirming the type and progression
CC   of cancer, and for drug screening and assays. The present sequence is a
CC   coding sequence of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub.published_pct_sequences.
XX
SQ   Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

  Query Match             63.9%;  Score 334.4;  DB 24;  Length 7260;
  Best Local Similarity   84.6%;  Pred. No. 5.7e-88;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 13
ABK84583
ID   ABK84583 standard; cDNA; 7260 BP.
XX
```

AC ABK84583;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #1154.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 1154; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)

CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 5.7e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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                || |||||| ||| ||||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 14
ABN97244
ID   ABN97244 standard; DNA; 7260 BP.
XX
AC   ABN97244;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Gene #3742 used to diagnose liver cancer.
XX
KW   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW   metastatic liver tumour; cytostatic; expression profile; disease state;
KW   disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS   Homo sapiens.
XX
PN   WO200229103-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US30589.
XX
PR   02-OCT-2000; 2000US-237054P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Horne D,  Alvares C,  Peres-Da-Silva S,  Vockley JG;
XX
DR   WPI; 2002-426119/45.
XX
PT   Diagnosing and detecting the progression of liver cancer,
PT   hepatocellular carcinoma or metastatic liver tumor in a patient,
PT   involves detecting the level of expression of two or more genes in a
PT   liver tissue sample  -
XX
PS   Claim 1; SEQ ID NO 3742; 298pp; English.
XX
CC   The invention relates to a novel method for diagnosing and detecting the
CC   progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC   tumour in a patient, and differentiating metastatic liver cancer from
CC   hepatocellular carcinoma in a patient, involving detecting the level of
CC   expression of two or more genes represented in ABN93503-ABN97455 in a
CC   tissue sample. The method of the invention has hepatotropic, and
CC   cytostatic activity. The method is useful for diagnosing and detecting
CC   the progression of liver cancer, hepatocellular carcinoma and metastatic
CC   liver carcinoma in a patient. The method is useful for identifying
CC   expression profiles which serve as useful diagnostic markers as well as
CC   markers that can be used to monitor disease states, disease progression,
CC   drug toxicity, drug efficacy and drug metabolism.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
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```
SQ   Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

  Query Match             63.9%;  Score 334.4;  DB 24;  Length 7260;
  Best Local Similarity   84.6%;  Pred. No. 5.7e-88;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| ||| ||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 15
ABK64812
ID   ABK64812 standard; DNA; 7260 BP.
XX
AC   ABK64812;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human benign prostatic hyperplasia gene #707.
XX
KW   Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS   Homo sapiens.
XX
```

PN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure; Page 391-393; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 5.7e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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                ||||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
                ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
                || |||||||||||||| || ||| |||| ||||| |||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
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Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 523
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	523	100.0	553	3	US-09-142-583A-3	Sequence 3, Appli
2	523	100.0	553	3	US-09-142-583A-5	Sequence 5, Appli
3	332.8	63.6	777	3	US-09-142-583A-10	Sequence 10, Appl
4	331.2	63.3	622	6	5405942-2	Patent No. 5405942
5	274.6	52.5	5707	2	US-08-472-809B-8	Sequence 8, Appli
6	274.6	52.5	6345	2	US-08-472-809B-7	Sequence 7, Appli
7	234.4	44.8	357	6	5405942-13	Patent No. 5405942
8	232.8	44.5	357	6	5405942-9	Patent No. 5405942
9	191.4	36.6	210	6	5405942-7	Patent No. 5405942
10	191.4	36.6	210	6	5405942-11	Patent No. 5405942
11	191.4	36.6	2862	4	US-09-255-829-13	Sequence 13, Appl

12	189.8	36.3	210	6	5405942-15	Patent No. 5405942
13	185.2	35.4	240	1	US-08-308-196A-1	Sequence 1, Appli
14	185.2	35.4	240	5	PCT-US91-06452-1	Sequence 1, Appli
15	185.2	35.4	390	3	US-09-029-267-13	Sequence 13, Appl
16	158.8	30.4	798	1	US-07-953-230A-6	Sequence 6, Appli
17	154.8	29.6	770	1	US-07-953-230A-1	Sequence 1, Appli
18	154.8	29.6	846	1	US-07-953-230A-5	Sequence 5, Appli
19	127	24.3	621	3	US-08-989-251-40	Sequence 40, Appl
20	127	24.3	621	3	US-09-340-250-40	Sequence 40, Appl
21	127	24.3	621	4	US-09-528-108-40	Sequence 40, Appl
22	125.8	24.1	233	1	US-08-444-142-3	Sequence 3, Appli
23	125.8	24.1	233	1	US-08-444-131-3	Sequence 3, Appli
24	125.8	24.1	485	1	US-07-989-845-29	Sequence 29, Appl
25	125.8	24.1	485	1	US-07-989-844-13	Sequence 13, Appl
26	125.8	24.1	485	1	US-08-110-663-1	Sequence 1, Appli
27	125.8	24.1	485	1	US-08-169-688-1	Sequence 1, Appli
28	125.8	24.1	485	1	US-08-240-121-13	Sequence 13, Appl
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33	125.8	24.1	485	1	US-08-470-108-1	Sequence 1, Appli
34	125.8	24.1	485	5	PCT-US93-11297-13	Sequence 13, Appl
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36	125.6	24.0	243	2	US-08-482-182-75	Sequence 75, Appl
37	124.2	23.7	717	1	US-08-284-784-40	Sequence 40, Appl
38	124.2	23.7	717	2	US-08-854-811-40	Sequence 40, Appl
39	124.2	23.7	783	1	US-08-284-784-43	Sequence 43, Appl
40	124.2	23.7	783	2	US-08-854-811-43	Sequence 43, Appl
41	124.2	23.7	891	1	US-08-284-784-33	Sequence 33, Appl
42	124.2	23.7	891	1	US-08-284-784-34	Sequence 34, Appl
43	124.2	23.7	891	2	US-08-854-811-33	Sequence 33, Appl
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ALIGNMENTS

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RESULT 1
US-09-142-583A-3
; Sequence 3, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;        APPLICANT: GOLDSPINK, GEOFFREY
;        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
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;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/142,583A
;              FILING DATE: 29-Oct-1998
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: WO PCT/GB97/00658
;              FILING DATE: 11-MAR-1997
;              APPLICATION NUMBER: GB 9605124.8
;              FILING DATE: 11-MAR-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SADOFF, B. J.
;              REGISTRATION NUMBER: 36663
;              REFERENCE/DOCKET NUMBER: 117-263
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 7038164000
;              TELEFAX: 7038164100
;    INFORMATION FOR SEQ ID NO: 3:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 553 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: both
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION: 1..363
;         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

  Query Match             100.0%;  Score 523;  DB 3;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-154;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db        211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db        391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Db        511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553


RESULT 2
US-09-142-583A-5
; Sequence 5, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;        APPLICANT: GOLDSPINK, GEOFFREY
;        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/142,583A
;             FILING DATE: 29-Oct-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: WO PCT/GB97/00658
;             FILING DATE: 11-MAR-1997
;             APPLICATION NUMBER: GB 9605124.8
;             FILING DATE: 11-MAR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B. J.
;             REGISTRATION NUMBER: 36663
;             REFERENCE/DOCKET NUMBER: 117-263
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 7038164000
;             TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 553 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: linear
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;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION: 341..397
;         SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

  Query Match             100.0%;  Score 523;  DB 3;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-154;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db         31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db        211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db        271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db        451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 3
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; Sequence 10, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;         APPLICANT: GOLDSPINK, GEOFFREY
;         TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;         NUMBER OF SEQUENCES: 11
;         CORRESPONDENCE ADDRESS:
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;              ADDRESSEE: NIXON & VANDERHYE P.C.
;              STREET: 1100 NORTH GLEBE ROAD
;              CITY: ARLINGTON
;              STATE: VA
;              COUNTRY: USA
;              ZIP: 22201
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/142,583A
;              FILING DATE: 29-Oct-1998
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: WO PCT/GB97/00658
;              FILING DATE: 11-MAR-1997
;              APPLICATION NUMBER: GB 9605124.8
;              FILING DATE: 11-MAR-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SADOFF, B. J.
;              REGISTRATION NUMBER: 36663
;              REFERENCE/DOCKET NUMBER: 117-263
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 7038164000
;              TELEFAX: 7038164100
;    INFORMATION FOR SEQ ID NO: 10:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 777 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: both
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION: 26..493
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US-09-142-583A-10

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  Matches  444;  Conservative    0;  Mismatches   27;  Indels   55;  Gaps    4;

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Db        179 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 238

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        239 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db        299 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db        419 ATGCCCAAGACCCAG---------------------------------------------- 433

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db        434 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 486

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
                |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        487 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 546

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
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RESULT 4
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;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:2:
;      LENGTH: 622
5405942-2

  Query Match             63.3%;  Score 331.2;  DB 6;  Length 622;
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  Matches  359;  Conservative   84;  Mismatches   28;  Indels   55;  Gaps    4;

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Db         45 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 104

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db        105 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 164

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||  |:||:|||:|||:||:||::||||||||:|:|||:|  |||||||:|||||:|:|
Db        165 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCAUAGGAGGCUGGAGAUGUAU 224
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Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              :| |||||||:|||||| || ||| |||| |||:| |:|||:||||||||||||||||||
Db        225 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 284

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |:||||||||| |||
Db        285 AUGCCCAAGACCCAG---------------------------------------------- 299

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||:|||:::|||||||  ||||:||||||||:|||||||||||||||:|
Db        300 -------AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUA 352

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db        353 CAGGAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCCACCGCAGGAUCCUUUG 412

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |:|:|||| ||::|||:| :|||| ::|||| ||| ||||||||:|||:::||: |||:
Db        413 CUCUGCACGAGUUACCUGUUAAACUUUGGAACACCUACCAAAAAAUAAGUUUGAUAACAU 472

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              :: |||||: ||| :::|||||||:||||:|||||||:||||::|
Db        473 UUAAAAGAUGGGCGUUUCCCCCAAUGAAAUACACAAGUAAACAUUC 518
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RESULT 5
US-08-472-809B-8
; Sequence 8, Application US/08472809B
; Patent No. 5925564
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: DeMayo, Franco J.
; APPLICANT: O'Malley, Bert W.
; TITLE OF INVENTION: Expression Vector Systems and
; TITLE OF INVENTION: Method of Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,809B
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,846

```
;       FILING DATE:  March 9, 1994
;       APPLICATION NUMBER:  07/789,919
;       FILING DATE:  No. 5925564ember 6, 1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  214/212
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5707 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-472-809B-8

  Query Match            52.5%;  Score 274.6;  DB 2;  Length 5707;
  Best Local Similarity  82.2%;  Pred. No. 5.3e-76;
  Matches  351;  Conservative    0;  Mismatches   24;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        853 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 912

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db       1033 ATGCCCAAGACCCAG---------------------------------------------- 1047

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1048 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 1100

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||   |
Db       1101 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 1160

Qy        421 CTCTGCA 427
                |||||
Db       1161 GGCTGCA 1167
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RESULT 6
US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564
;  GENERAL INFORMATION:
;    APPLICANT:  Schwartz, Robert J.
;    APPLICANT:  DeMayo, Franco J.
;    APPLICANT:  O'Malley, Bert W.
;    TITLE OF INVENTION:  Expression Vector Systems and
;    TITLE OF INVENTION:  Method of Use
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,809B
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/209,846
;      FILING DATE:  March 9, 1994
;      APPLICATION NUMBER:  07/789,919
;      FILING DATE:  No. 5925564ember 6, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  214/212
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6345 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-472-809B-7

  Query Match             52.5%;  Score 274.6;  DB 2;  Length 6345;
  Best Local Similarity   82.2%;  Pred. No. 5.6e-76;
  Matches  351;  Conservative    0;  Mismatches   24;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
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Db       3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db       3762 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 3821

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db       3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 3941

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||
Db       3942 ATGCCCAAGACCCAG---------------------------------------------- 3956

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       3957 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||   |
Db       4010 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 4069

Qy        421 CTCTGCA 427
                |||||
Db       4070 GGCTGCA 4076
```

RESULT 7
5405942-13
;Patent No. 5405942
; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/65,673
;   FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 630,557
;   FILING DATE: 19-JUL-1984
;SEQ ID NO:13:
;   LENGTH: 357
5405942-13

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  Query Match            44.8%;  Score 234.4;  DB 6;  Length 357;
  Best Local Similarity  93.8%;  Pred. No. 5.1e-64;
  Matches  244;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102
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Qy          61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
               |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db         103 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162

Qy         121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy         181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
               || |||||||||| ||| || ||| |||| ||||| ||||||||||||||||||||||||
Db         223 TGCGCACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 282

Qy         241 ATGCCCAAGACTCAGAAGTA 260
               |||||||||| |||||| |
Db         283 ATGCCCAAGACCCAGAAGGA 302
```

RESULT 8
5405942-9
;Patent No. 5405942
; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/65,673
;   FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 630,557
;   FILING DATE: 19-JUL-1984
;SEQ ID NO:9:
;   LENGTH: 357
5405942-9

Query Match 44.5%; Score 232.8; DB 6; Length 357;
Best Local Similarity 76.5%; Pred. No. 1.6e-63;
Matches 199; Conservative 44; Mismatches 17; Indels 0; Gaps 0;

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Qy           1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
               |||||||||||||:|:|||| ||:||||:||:||| ||:|::|||::||:|:|:||||||
Db          43 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC 102

Qy          61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
               ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db         103 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 162

Qy         121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
               ||||| |:||:|||:|||:||:| ::||||||||:|:||:|: |||||||:||||||:|:|
Db         163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222

Qy         181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
               :| |||||||:|||||| || ||| |||| |||:| |:|||:||||||||||||||||||
Db         223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 282

Qy         241 ATGCCCAAGACTCAGAAGTA 260
               |:|||||||| |||||| |
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Db        283 AUGCCCAAGACCCAGAAGGA 302


RESULT 9
5405942-7
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:7:
;      LENGTH: 210
5405942-7

  Query Match             36.6%;  Score 191.4;  DB 6;  Length 210;
  Best Local Similarity   75.1%;  Pred. No. 1.2e-50;
  Matches  157;  Conservative   41;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||:|:|||| ||:||||:||:|||:||:|::|||::||:|:|:||||||
Db          1 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db         61 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |:||:|||:|||:||:||::|||||||:|:||:|: |||||||:|||||:|:|
Db        121 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              :| |||||||:|||||| || ||| ||||
Db        181 UGCGCACCCCUCAAGCCUGCCAAGUCAGC 209


RESULT 10
5405942-11
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:11:
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; LENGTH: 210
5405942-11

  Query Match 36.6%; Score 191.4; DB 6; Length 210;
  Best Local Similarity 94.7%; Pred. No. 1.2e-50;
  Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              || |||||||||||||| || ||| ||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 209
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RESULT 11
US-09-255-829-13
; Sequence 13, Application US/09255829
; Patent No. 6461617
; GENERAL INFORMATION:
;   APPLICANT: Shone, Clifford Charles
;   APPLICANT: Quinn, Conrad Padraig
;   APPLICANT: Foster, Keith Alan
;   TITLE OF INVENTION: Recombinant Toxin Fragments
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
;   STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
;   CITY: WASHINGTON
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005-3934
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/255,829
;   FILING DATE: 23-FEB-1999
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB97/02273
;   FILING DATE: 22-AUG-1997
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/782,893
;   FILING DATE: 27-DEC-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: ESMOND, ROBERT W.

```
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1581.0130002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2862 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..2862
US-09-255-829-13

  Query Match             36.6%;  Score 191.4;  DB 4;  Length 2862;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-50;
  Matches  198;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db       2704 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 2763

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              || |||||||||||||| || ||| ||||
Db       2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 2852


RESULT 12
5405942-15
;Patent No. 5405942
;     APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;     TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;     NUMBER OF SEQUENCES: 16
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/65,673
;       FILING DATE: 16-JUN-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 630,557
;       FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
;       LENGTH: 210
5405942-15

  Query Match             36.3%;  Score 189.8;  DB 6;  Length 210;
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  Best Local Similarity   74.6%;  Pred. No. 3.8e-50;
  Matches  156;  Conservative   41;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||:|:|||| ||:||||:||:|||:||:|::|||::||:|:|:||||||
Db          1 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db         61 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |:||:|||:|||:||:||::|||||||:|:||:|: |||||||:|||||:|:|
Db        121 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              :| |||||||:|| ||| || ||| ||||
Db        181 UGCGCACCCCUCAGGCCUGCCAAGUCAGC 209


RESULT 13
US-08-308-196A-1
; Sequence 1, Application US/08308196A
; Patent No. 5612198
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Howard, Bradley D.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,196A
;      FILING DATE:  09-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,523
;      FILING DATE:  03-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/578,728
;      FILING DATE:  04-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
```

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;       REFERENCE/DOCKET NUMBER:  51875
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619)238-0999
;       TELEFAX:  (619)238-0062
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  240 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  14..232
US-08-308-196A-1

  Query Match             35.4%;  Score 185.2;  DB 1;  Length 240;
  Best Local Similarity   91.6%;  Pred. No. 1.1e-48;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

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Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
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RESULT 14
PCT-US91-06452-1
; Sequence 1, Application PC/TUS9106452
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Bradley, D. H.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 South LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US91/06452
;       FILING DATE:  19910409
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/578,728
;       FILING DATE:  04-SEP-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie L.
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  51874
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619)552-1311
;       TELEFAX:  (619)552-0095
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  240 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  14..232
PCT-US91-06452-1

  Query Match             35.4%;  Score 185.2;  DB 5;  Length 240;
  Best Local Similarity   91.6%;  Pred. No. 1.1e-48;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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RESULT 15
US-09-029-267-13
; Sequence 13, Application US/09029267
; Patent No. 6107057
;  GENERAL INFORMATION:
;    APPLICANT:  Crawford, Kenneth
;    APPLICANT:  Zaror, Isabel
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;     APPLICANT:  Innis, Michael
;     TITLE OF INVENTION:  Pichia Secretory Leader for Protein
;     TITLE OF INVENTION:  Expression
;     NUMBER OF SEQUENCES:  40
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Chiron Corporation
;       STREET:  4560 Horton Street
;       CITY:  Emeryville
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  94608
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/029,267
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Chung, Ling-Fong
;       REGISTRATION NUMBER:  36,482
;       REFERENCE/DOCKET NUMBER:  1165.100
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 601-2704
;       TELEFAX:  (510) 655-3542
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  390 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "Synthetic"
US-09-029-267-13
  Query Match             35.4%;  Score 185.2;  DB 3;  Length 390;
  Best Local Similarity   91.6%;  Pred. No. 1.5e-48;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Job time : 49.3585 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:29:55 ; Search time 233.512 Seconds
(without alignments)
7443.919 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

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	3	409	78.2	471	9	US-09-852-261-13	Sequence 13, Appl
	4	356.8	68.2	539	9	US-09-852-261-3	Sequence 3, Appli
	5	349.4	66.8	651	15	US-10-161-088-1	Sequence 1, Appli
	6	334.4	63.9	7260	10	US-09-919-497-24	Sequence 24, Appl
	7	334.4	63.9	7260	10	US-09-880-107-3739	Sequence 3739, Ap
	8	334.4	63.9	7260	13	US-09-873-319-707	Sequence 707, App
	9	334.4	63.9	7260	13	US-09-960-706-1066	Sequence 1066, Ap
	10	334.4	63.9	7260	15	US-10-136-639-4	Sequence 4, Appli
	11	332.8	63.6	725	15	US-10-207-655-54	Sequence 54, Appl
	12	273.6	52.3	612	13	US-10-251-661-7	Sequence 7, Appli
	13	262	50.1	487	9	US-09-852-261-11	Sequence 11, Appl
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	16	209	40.0	286	15	US-10-161-088-3	Sequence 3, Appli
	17	193	36.9	210	13	US-09-807-742-18	Sequence 18, Appl
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	20	186.6	35.7	210	10	US-09-930-377B-2	Sequence 2, Appli
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	24	141.6	27.1	213	15	US-10-076-816-9	Sequence 9, Appli
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	26	127	24.3	621	9	US-09-921-398-40	Sequence 40, Appl
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	29	113.4	21.7	480	15	US-10-280-826-38	Sequence 38, Appl
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c	33	75.4	14.4	447	10	US-09-833-263-917	Sequence 917, App
c	34	75.4	14.4	447	14	US-10-025-380-917	Sequence 917, App
c	35	75.2	14.4	437	15	US-10-066-543-663	Sequence 663, App
c	36	75.2	14.4	493	15	US-10-066-543-997	Sequence 997, App
c	37	75.2	14.4	518	15	US-10-066-543-1040	Sequence 1040, Ap
c	38	75.2	14.4	536	15	US-10-066-543-428	Sequence 428, App
	39	75.2	14.4	543	15	US-10-136-841-1	Sequence 1, Appli
c	40	75.2	14.4	549	15	US-10-066-543-478	Sequence 478, App
c	41	75.2	14.4	574	9	US-09-922-217-918	Sequence 918, App
c	42	75.2	14.4	574	10	US-09-833-263-918	Sequence 918, App
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c	44	75.2	14.4	577	15	US-10-066-543-1137	Sequence 1137, Ap
c	45	75.2	14.4	579	15	US-10-066-543-1094	Sequence 1094, Ap

ALIGNMENTS

RESULT 1
US-09-852-261-5
; Sequence 5, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY

```
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
US-09-852-261-5

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  Best Local Similarity   100.0%;  Pred. No. 1.9e-161;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

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Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

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Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 2
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US-09-852-261-1
; Sequence 1, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-1

Query Match 89.4%; Score 467.4; DB 9; Length 517;
Best Local Similarity 96.2%; Pred. No. 3.8e-143;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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RESULT 3
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; Sequence 13, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
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;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

  Query Match             78.2%;  Score 409;  DB 9;  Length 471;
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Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368
```

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Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471
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RESULT 4
US-09-852-261-3
; Sequence 3, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-3

Query Match 68.2%; Score 356.8; DB 9; Length 539;
Best Local Similarity 82.3%; Pred. No. 9.9e-107;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| ||||||||||||||| || |||||||||| |||||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  |||||| ||||| |||| || ||| |||| |||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
```

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Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
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RESULT 5
US-10-161-088-1
; Sequence 1, Application US/10161088
; Publication No. US20030077761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT: Rosengren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-111001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(471)
US-10-161-088-1

Query Match 66.8%; Score 349.4; DB 15; Length 651;
Best Local Similarity 82.8%; Pred. No. 3e-104;
Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||| ||||||||||||
Db        259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  |||||||||||||||||| |||
Db        319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378
```

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Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| | || |||  |||      || |||||||   ||
Db        559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
              ||||| ||||||| ||||||||||||||||||
Db        619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651
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RESULT 6
US-09-919-497-24
; Sequence 24, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-24

Query Match 63.9%; Score 334.4; DB 10; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
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```
Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 7
US-09-880-107-3739
; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

Query Match 63.9%; Score 334.4; DB 10; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 8
US-09-873-319-707
; Sequence 707, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; CURRENT FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 707

; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 X57025
US-09-873-319-707

Query Match 63.9%; Score 334.4; DB 13; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||| ||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 9
US-09-960-706-1066
; Sequence 1066, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using
; TITLE OF INVENTION: Gene Expression Profiles

; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1066
;   LENGTH: 7260
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066

  Query Match   63.9%; Score 334.4; DB 13; Length 7260;
  Best Local Similarity   84.6%; Pred. No. 9e-99;
  Matches 445; Conservative   0; Mismatches   26; Indels   55; Gaps   4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  ||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 10
US-10-136-639-4
; Sequence 4, Application US/10136639
; Publication No. US20030072761A1
; GENERAL INFORMATION:
; APPLICANT: LeBowitz, Jonathan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLOOD BRAIN
; TITLE OF INVENTION: BARRIER
; FILE REFERENCE: SYM-008
; CURRENT APPLICATION NUMBER: US/10/136,639
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 60/329,650
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-136-639-4

Query Match 63.9%; Score 334.4; DB 15; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||||| ||||
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Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 11
US-10-207-655-54
; Sequence 54, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
;   LENGTH: 725
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-54

  Query Match             63.6%;  Score 332.8;  DB 15;  Length 725;
  Best Local Similarity   84.4%;  Pred. No. 9.2e-99;
  Matches  444;  Conservative    0;  Mismatches  27;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        156 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 215

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        216 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| |||||||||||||||||||||||
Db        336 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 395

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        396 ATGCCCAAGACCCAG---------------------------------------------- 410

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        411 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 463

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        464 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 523
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Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  ||||||||||||||||| ||||
Db        524 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 583

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| |||||||||||||||||||||||||||||||
Db        584 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 629


RESULT 12
US-10-251-661-7
; Sequence 7, Application US/10251661
; Publication No. US20030166555A1
; GENERAL INFORMATION:
;  APPLICANT: Alberini, Cristina M.
;  APPLICANT:  Bear, Mark F.
;  TITLE OF INVENTION: Methods and Compositions for Regulating
;  TITLE OF INVENTION:  Memory Consolidation
;  FILE REFERENCE: 3499.1001-003
;  CURRENT APPLICATION NUMBER: US/10/251,661
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/193,614
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US01/10661
;  PRIOR FILING DATE: 2001-04-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (151)...(564)
US-10-251-661-7

  Query Match             52.3%;  Score 273.6;  DB 13;  Length 612;
  Best Local Similarity   83.0%;  Pred. No. 2.6e-79;
  Matches  347;  Conservative    0;  Mismatches   19;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        247 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 306

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db        307 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 366

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        367 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 426

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        427 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 486
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Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        487 ATGCCCAAGACCCAG---------------------------------------------- 501

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        502 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 554

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTT 418
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||
Db        555 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612


RESULT 13
US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-852-261-11

  Query Match             50.1%;  Score 262;  DB 9;  Length 487;
  Best Local Similarity   74.7%;  Pred. No. 1.5e-75;
  Matches  396;  Conservative    0;  Mismatches   75;  Indels   59;  Gaps    3;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| ||||||||||||||||  || |||||||||| |||||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| ||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255
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Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                  |||||||||||| |||||||||||||||||||| |||||||||||||||| |||
Db        256 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        309 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        369 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        429 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 478
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RESULT 14
US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-9

Query Match 45.4%; Score 237.6; DB 9; Length 318;
Best Local Similarity 94.6%; Pred. No. 1.3e-67;
Matches 246; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
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Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTA 260
              |||||||||||  ||||||  |
Db        241 ATGCCCAAGACCCAGAAGGA 260


RESULT 15
US-10-238-114-1
; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
;  APPLICANT: Merial
;  APPLICANT:  ANDREONI , Christine Michele
;  TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST
FELINE RETROVIRUS
;  FILE REFERENCE: 454313-3165.1
;  CURRENT APPLICATION NUMBER: US/10/238,114
;  CURRENT FILING DATE:  2002-09-10
;  PRIOR APPLICATION NUMBER: FR 01 11736
;  PRIOR FILING DATE: 2001-09-11
;  PRIOR APPLICATION NUMBER: US 60/318,666
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-238-114-1

  Query Match             43.6%;  Score 228;  DB 15;  Length 462;
  Best Local Similarity   92.3%;  Pred. No. 2.3e-64;
  Matches  240;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||  ||||||||||| ||  ||||||  |||||||  ||||||||||||||||||||||||
Db        145 GGACCAGAGACGCTCTGTGGGGCTGAGTTGGTGGACGCTCTTCAGTTCGTGTGTGGAGAC 204

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||  |||||||||||||||||||  ||  ||  ||||||||||||||||||||||||||
Db        205 AGGGGTTTTTATTTCAACAAGCCCACGGGGTATGGCTCCAGCAGTCGGAGGGCACCTCAG 264

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||  |||||||||
Db        265 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGCGGCTAGAGATGTAC 324

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||  ||  |||  |  ||||||||  ||||||||  ||||||||||  |||
Db        325 TGTGCACCCCTCAAGCCTGCCAAGTCTGCCCGCTCAGTCCGTGCTCAGCGCCACACTGAC 384

Qy        241 ATGCCCAAGACTCAGAAGTA 260
              |||||||||  ||||||||  |
Db        385 ATGCCCAAGGCTCAGAAGGA 404

Search completed: December 13, 2003, 11:56:48
Job time : 235.512 secs
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